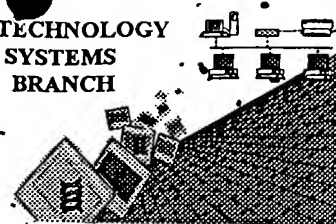


0590

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/057,834  
Source: OTPE  
Date Processed by STIC: 2/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

## Raw Sequence Listing Error Summary .

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 10/057,834

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                                  prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                                  ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                                  each n or Xaa can only represent a single residue. Please present the maximum number of each  
                                  residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)       . Normally, PatentIn would automatically generate this section from the  
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                  the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                                  Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                                  is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)   Z1   missing the <220> "Feature" and associated numeric identifiers and responses.  
                                  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                                  "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed

*see additional page*



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,834

DATE: 02/15/2002

TIME: 14:10:04

Input Set : A:\Arcd358.app

Output Set: N:\CRF3\02152002\J057834.raw

```

3 <110> APPLICANT: RATAIN, MARK J.
4     INNOCENTI, FEDERICO
5     DAS, SOMA
6     IYER, LALITHA
7     SAWYER, MICHAEL
9 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OPTIMIZING UGT2B7 SUBSTRATE
DOSINGS AND FOR
10    PREDICTING UGT2B7 SUBSTRATE TOXICITY
12 <130> FILE REFERENCE: ARCD:358US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/057,834
C--> 14 <141> CURRENT FILING DATE: 2002-01-25
14 <150> PRIOR APPLICATION NUMBER: UNKNOWN
15 <151> PRIOR FILING DATE: 2002-01-25
W--> 17 <140> CURRENT APPLICATION NUMBER: 60/264,534
C--> 18 <141> CURRENT FILING DATE: 2001-01-26
21 <160> NUMBER OF SEQ ID NOS: 78
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1991
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (151)..(1740)
34 <400> SEQUENCE: 1
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37 taactttcttg gctaatttat ctttggacat aaccatgaga aatgacagaa aggaacagca 120
39 actggaaaac aagcattgca ttgcaccagg atg tct gtg aaa tgg act tca gta 174
40                                     Met Ser Val Lys Trp Thr Ser Val
41                                     1           5
43 att ttg cta ata caa ctg agc ttt tgc ttt agc tct ggg aat tgt gga 222
44 Ile Leu Leu Ile Gln Leu Ser Phe Cys Phe Ser Ser Gly Asn Cys Gly
45     10           15           20
47 aag gtg ctg gtg tgg gca gca gaa tac agc cat tgg atg aat ata aag 270
48 Lys Val Leu Val Trp Ala Ala Glu Tyr Ser His Trp Met Asn Ile Lys
49 25           30           35           40
51 aca atc ctg gat gag ctt att cag aga ggt cat gag gtg act gta ctg 318
52 Thr Ile Leu Asp Glu Leu Ile Gln Arg Gly His Glu Val Thr Val Leu
53           45           50           55
55 gca tct tca gct tcc att ctt ttt gat ccc aac aac tca tcc gct ctt 366
56 Ala Ser Ser Ala Ser Ile Leu Phe Asp Pro Asn Asn Ser Ser Ala Leu
57           60           65           70
59 aaa att gaa att tat ccc aca tct tta act aaa act gag ttg gag aat 414
60 Lys Ile Glu Ile Tyr Pro Thr Ser Leu Thr Lys Thr Glu Leu Glu Asn

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,834

DATE: 02/15/2002

TIME: 14:10:04

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Output Set: N:\CRF3\02152002\J057834.raw

61	75	80	85	
63	ttc atc atg caa cag att aag aga tgg tca gac ctt cca aaa gat aca	462		
64	Phe Ile Met Gln Gln Ile Lys Arg Trp Ser Asp Leu Pro Lys Asp Thr			
65	90 95 100			
67	ttt tgg tta tat ttt tca caa gta cag gaa atc atg tca ata ttt ggt	510		
68	Phe Trp Leu Tyr Phe Ser Gln Val Gln Glu Ile Met Ser Ile Phe Gly			
69	105 110 115 120			
71	gac ata act aga aag ttc tgt aaa gat gta gtt tca aat aag aaa ttt	558		
72	Asp Ile Thr Arg Lys Phe Cys Lys Asp Val Val Ser Asn Lys Lys Phe			
73	125 130 135			
75	atg aaa aaa gta caa gag tca aga ttt gac gtc att ttt gca gat gct	606		
76	Met Lys Lys Val Gln Glu Ser Arg Phe Asp Val Ile Phe Ala Asp Ala			
77	140 145 150			
79	att ttt ccc tgt agt gag ctg ctg gct gag cta ttt aac ata ccc ttt	654		
80	Ile Phe Pro Cys Ser Glu Leu Leu Ala Glu Leu Phe Asn Ile Pro Phe			
81	155 160 165			
83	gtg tac agt ctc agc ttc tct cct ggc tac act ttt gaa aag cat agt	702		
84	Val Tyr Ser Leu Ser Phe Ser Pro Gly Tyr Thr Phe Glu Lys His Ser			
85	170 175 180			
87	gga gga ttt att ttc cct cct tcc tac gta cct gtt gtt atg tca gaa	750		
88	Gly Gly Phe Ile Phe Pro Pro Ser Tyr Val Pro Val Val Met Ser Glu			
89	185 190 195 200			
91	tta act gat caa atg act ttc atg gag agg gta aaa aat atg atc tat	798		
92	Leu Thr Asp Gln Met Thr Phe Met Glu Arg Val Lys Asn Met Ile Tyr			
93	205 210 215			
95	gtg ctt tac ttt gac ttt tgg ttc gaa ata ttt gac atg aag aag tgg	846		
96	Val Leu Tyr Phe Asp Phe Trp Phe Glu Ile Phe Asp Met Lys Lys Trp			
97	220 225 230			
99	gat cag ttt tat agt gaa gtt cta gga aga ccc act acg tta tct gag	894		
100	Asp Gln Phe Tyr Ser Glu Val Leu Gly Arg Pro Thr Thr Leu Ser Glu			
101	235 240 245			
103	aca atg ggg aaa gct gac gta tgg ctt att cga aac tcc tgg aat ttt	942		
104	Thr Met Gly Lys Ala Asp Val Trp Leu Ile Arg Asn Ser Trp Asn Phe			
105	250 255 260			
107	cag ttt cct cat cca ctc tta cca aat gtt gat ttt gtt gga gga ctc	990		
108	Gln Phe Pro His Pro Leu Leu Pro Asn Val Asp Phe Val Gly Gly Leu			
109	265 270 275 280			
111	cac tgc aaa cct gcc aaa ccc ctg cct aag gaa atg gaa gac ttt gta	1038		
112	His Cys Lys Pro Ala Lys Pro Leu Pro Lys Glu Met Glu Asp Phe Val			
113	285 290 295			
115	cag agc tct gga gaa aat ggt gtt gtg gtg ttt tct ctg ggg tca atg	1086		
116	Gln Ser Ser Gly Glu Asn Gly Val Val Val Phe Ser Leu Gly Ser Met			
117	300 305 310			
119	gtc agt aac atg aca gaa gaa agg gcc aac gta att gca tca gcc ctg	1134		
120	Val Ser Asn Met Thr Glu Glu Arg Ala Asn Val Ile Ala Ser Ala Leu			
121	315 320 325			
123	gcc cag atc cca caa aag gtt ctg tgg aga ttt gat ggg aat aaa cca	1182		
124	Ala Gln Ile Pro Gln Lys Val Leu Trp Arg Phe Asp Gly Asn Lys Pro			
125	330 335 340			

## RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/057,834

TIME: 14:10:04

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Output Set: N:\CRF3\02152002\J057834.raw

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127 gat acc tta ggt ctc aat act cgg ctg tat aag tgg ata ccc cag aat 1230
128 Asp Thr Leu Gly Leu Asn Thr Arg Leu Tyr Lys Trp Ile Pro Gln Asn
129 345 350 355 360
131 gac ctt cta ggt cat cca aag acc aga gct ttt ata act cat ggt gga 1278
132 Asp Leu Leu Gly His Pro Lys Thr Arg Ala Phe Ile Thr His Gly Gly
133 365 370 375
135 gcc aat ggc atc tac gag gca atc tac cat ggg atc cct atg gtg ggg 1326
136 Ala Asn Gly Ile Tyr Glu Ala Ile Tyr His Gly Ile Pro Met Val Gly
137 380 385 390
139 att cca ttg ttt gcc gat caa cct gat aac att gct cac atg aag gcc 1374
140 Ile Pro Leu Phe Ala Asp Gln Pro Asp Asn Ile Ala His Met Lys Ala
141 395 400 405
143 agg gga gca gct gtt aga gtg gac ttc aac aca atg tgg agt aca gac 1422
144 Arg Gly Ala Ala Val Arg Val Asp Phe Asn Thr Met Ser Ser Thr Asp
145 410 415 420
147 ttg ctg aat gca ttg aag aga gta att aat gat cct tca tat aaa gag 1470
148 Leu Leu Asn Ala Leu Lys Arg Val Ile Asn Asp Pro Ser Tyr Lys Glu
149 425 430 435 440
151 aat gtt atg aaa tta tca aga att caa cat gat caa cca gtg aag ccc 1518
152 Asn Val Met Lys Leu Ser Arg Ile Gln His Asp Gln Pro Val Lys Pro
153 445 450 455
155 ctg gat cga gca gtc ttc tgg att gaa ttt gtc atg cgc cac aaa gga 1566
156 Leu Asp Arg Ala Val Phe Trp Ile Glu Phe Val Met Arg His Lys Gly
157 460 465 470
159 gct aaa cac ctt cgg gtt gca gcc cac gac ctc acc tgg ttc cag tac 1614
160 Ala Lys His Leu Arg Val Ala Ala His Asp Leu Thr Trp Phe Gln Tyr
161 475 480 485
163 cac tct ttg gat gtg att ggg ttc ctg ctg gtc tgt gtg gca act gtg 1662
164 His Ser Leu Asp Val Ile Gly Phe Leu Leu Val Cys Val Ala Thr Val
165 490 495 500
167 ata ttt atc gtc aca aaa tgt tgt ctg ttt tgt ttc tgg aag ttt gct 1710
168 Ile Phe Ile Val Thr Lys Cys Cys Leu Phe Cys Phe Trp Lys Phe Ala
169 505 510 515 520
171 aga aaa gca aag aag gga aaa aat gat tag ttatatctga gatttgaagc 1760
172 Arg Lys Ala Lys Lys Gly Lys Asn Asp
W--> 173 525 530
175 tggaaaacct gataggtgag actacttcag tttattccag caagaaagat tgtgatgcaa 1820
177 gattttctttc ttcctgagac aaaaaaaaaa aaaagaaaaa aaaatctttt caaaatttac 1880
179 tttgtcaaat aaaaatttgt ttttcagaga tttaccaccc agttcatggt tagaaatatt 1940
181 ttgtggcaat gaagaaaaca ctacggaaaa taaaaaataa gataaagcct t 1991
184 <210> SEQ ID NO: 2
185 <211> LENGTH: 529
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 2
190 Met Ser Val Lys Trp Thr Ser Val Ile Leu Leu Ile Gln Leu Ser Phe
191 1 5 10 15
192 Cys Phe Ser Ser Gly Asn Cys Gly Lys Val Leu Val Trp Ala Ala Glu
193 20 25 30

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## RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/057,834

TIME: 14:10:04

Input Set : A:\Arcd358.app

Output Set: N:\CRF3\02152002\J057834.raw

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194 Tyr Ser His Trp Met Asn Ile Lys Thr Ile Leu Asp Glu Leu Ile Gln
195           35           40           45
196 Arg Gly His Glu Val Thr Val Leu Ala Ser Ser Ala Ser Ile Leu Phe
197           50           55           60
198 Asp Pro Asn Asn Ser Ser Ala Leu Lys Ile Glu Ile Tyr Pro Thr Ser
199   65           70           75           80
200 Leu Thr Lys Thr Glu Leu Glu Asn Phe Ile Met Gln Gln Ile Lys Arg
201           85           90           95
202 Trp Ser Asp Leu Pro Lys Asp Thr Phe Trp Leu Tyr Phe Ser Gln Val
203           100          105          110
204 Gln Glu Ile Met Ser Ile Phe Gly Asp Ile Thr Arg Lys Phe Cys Lys
205           115          120          125
206 Asp Val Val Ser Asn Lys Lys Phe Met Lys Lys Val Gln Glu Ser Arg
207   130           135          140
208 Phe Asp Val Ile Phe Ala Asp Ala Ile Phe Pro Cys Ser Glu Leu Leu
209  145           150          155          160
210 Ala Glu Leu Phe Asn Ile Pro Phe Val Tyr Ser Leu Ser Phe Ser Pro
211           165          170          175
212 Gly Tyr Thr Phe Glu Lys His Ser Gly Gly Phe Ile Phe Pro Pro Ser
213           180          185          190
214 Tyr Val Pro Val Val Met Ser Glu Leu Thr Asp Gln Met Thr Phe Met
215           195          200          205
216 Glu Arg Val Lys Asn Met Ile Tyr Val Leu Tyr Phe Asp Phe Trp Phe
217   210          215          220
218 Glu Ile Phe Asp Met Lys Lys Trp Asp Gln Phe Tyr Ser Glu Val Leu
219  225          230          235          240
220 Gly Arg Pro Thr Thr Leu Ser Glu Thr Met Gly Lys Ala Asp Val Trp
221           245          250          255
222 Leu Ile Arg Asn Ser Trp Asn Phe Gln Phe Pro His Pro Leu Leu Pro
223           260          265          270
224 Asn Val Asp Phe Val Gly Gly Leu His Cys Lys Pro Ala Lys Pro Leu
225           275          280          285
226 Pro Lys Glu Met Glu Asp Phe Val Gln Ser Ser Gly Glu Asn Gly Val
227   290          295          300
228 Val Val Phe Ser Leu Gly Ser Met Val Ser Asn Met Thr Glu Glu Arg
229  305          310          315          320
230 Ala Asn Val Ile Ala Ser Ala Leu Ala Gln Ile Pro Gln Lys Val Leu
231           325          330          335
232 Trp Arg Phe Asp Gly Asn Lys Pro Asp Thr Leu Gly Leu Asn Thr Arg
233           340          345          350
234 Leu Tyr Lys Trp Ile Pro Gln Asn Asp Leu Leu Gly His Pro Lys Thr
235           355          360          365
236 Arg Ala Phe Ile Thr His Gly Gly Ala Asn Gly Ile Tyr Glu Ala Ile
237   370          375          380
238 Tyr His Gly Ile Pro Met Val Gly Ile Pro Leu Phe Ala Asp Gln Pro
239  385          390          395          400
240 Asp Asn Ile Ala His Met Lys Ala Arg Gly Ala Ala Val Arg Val Asp
241           405          410          415
242 Phe Asn Thr Met Ser Ser Thr Asp Leu Leu Asn Ala Leu Lys Arg Val

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,834

DATE: 02/15/2002

TIME: 14:10:04

Input Set : A:\Arcd358.app

Output Set: N:\CRF3\02152002\J057834.raw

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243           420           425           430
244 Ile Asn Asp Pro Ser Tyr Lys Glu Asn Val Met Lys Leu Ser Arg Ile
245           435           440           445
246 Gln His Asp Gln Pro Val Lys Pro Leu Asp Arg Ala Val Phe Trp Ile
247           450           455           460
248 Glu Phe Val Met Arg His Lys Gly Ala Lys His Leu Arg Val Ala Ala
249 465           470           475           480
250 His Asp Leu Thr Trp Phe Gln Tyr His Ser Leu Asp Val Ile Gly Phe
251           485           490           495
252 Leu Leu Val Cys Val Ala Thr Val Ile Phe Ile Val Thr Lys Cys Cys
253           500           505           510
254 Leu Phe Cys Phe Trp Lys Phe Ala Arg Lys Ala Lys Lys Gly Lys Asn
255           515           520           525
256 Asp
260 <210> SEQ ID NO: 3
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
265 <400> SEQUENCE: 3
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269 <210> SEQ ID NO: 4
270 <211> LENGTH: 20
271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens
274 <400> SEQUENCE: 4
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280 <212> TYPE: DNA
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 5
284 cttggctaatt ttatcttttg                      20
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288 <211> LENGTH: 19
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <400> SEQUENCE: 6
293 cccactaccc tgactttat                      19
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 20
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 7
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306 <211> LENGTH: 19
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 8

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/057,834

DATE: 02/15/2002

TIME: 14:10:05

Input Set : A:\Arcd358.app

Output Set: N:\CRF3\02152002\J057834.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:17 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:17 M:281 W: Numeric Fields not Ordered, <140> not ordered!.  
L:17 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:18 M:281 W: Numeric Fields not Ordered, <141> not ordered!.  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:877 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:877 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:



## Additional Page

<210> 71  
<211> 20  
<212> DNA  
<213> Artificial Sequence )-  
<400> 71  
tctgagcatg tggatggcaa

Use of Artificial Sequence  
requires the use of numeric  
identifiers <220> and <223> <sup>20</sup>

See item # 11 on Error Summary  
Sheet